

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Cancel claims 1-18.

19. (New) An antibody or an antigen binding fragment thereof having the CDR-H3 sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31.

20. (New) An antibody or an antigen binding fragment thereof having the CDR-L3 sequence selected from the group consisting of: SEQ ID NO: 32, and SEQ ID NO: 34.

21. (New) An antibody or an antigen binding fragment thereof having a CDR-H3 sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31, and a CDR-L3 sequence selected from the group consisting of: SEQ ID NO: 32, and SEQ ID NO: 34.

22. (New) A method for identifying candidate sequences of at least the CDR3 region of antibodies specific against at least

one antigen produced by *Clostridium difficile* during an infection or against a vaccine, comprising the steps of:

(i) with B cells isolated from at least one patient who has been infected by *Clostridium difficile* or administered said vaccine, sequencing at least the CDR3 region of the VH and/or VL coding regions of said B cells; and

(ii) correlating said sequences of at least the CDR3 regions of the VH and/or VL coding regions of said B cells from said at least one patient to identify a set of candidate sequences for at least a CDR3 region of antibodies specific against said at least one antigen produced by *Clostridium difficile* or against said vaccine, each of said set of candidate CDR3 sequences or a sequence having at least 80% homology therewith occurring in total at a frequency of at least 1 percent in the set of sequences determined at step (i).

23. (New) A method according to claim 22, said B cells being selected from the group consisting of peripheral B-cell lymphocytes and B cells from the spleen.

24. (New) A method according to claim 23, said peripheral B-cell lymphocytes being isolated from blood from said at least one patient.

25. (New) A method according to claim 22, said at least one antigen being an immunogen.

26. (New) A method according to claim 22, said at least one patient displaying a pronounced antibody response in response to infection by *Clostridium difficile*.

27. (New) A method according to claim 22, said at least one patient having recovered from infection by *Clostridium difficile*.

28. (New) A method according to claim 22, said correlation step (ii) comprising determining putative amino acid sequences from said sequences of at least the VH and/or VL CDR3 coding regions, and correlating said putative amino acid sequences.

29. (New) A method according to claim 27, said correlation step (ii) comprising identifying the Complementarity Determining

Regions comprised in said at least the VH and/or VL regions and correlating said Complementarity Determining Regions.

30. (New) A method according to claim 29, said Complementarity Determining Regions being selected from the group consisting of CDR1, CDR2 and CDR3.

31. (New) A method according to claim 22, said correlation step (ii) additionally correlating at least one of the group consisting of: the strain of *Clostridium difficile* infecting said at least one patient, the time point at which said B cells are isolated during infection of said at least one patient by *Clostridium difficile*, the age of said at least one patient, the sex of said at least one patient, and the race of said at least one patient.

32. (New) A method according to claim 22, said B cells having been isolated from said at least one patient at a plurality of time points during infection of said at least one patient by *Clostridium difficile*, said correlation step (ii) correlating the time point during infection of said at least one patient by *Clostridium difficile* at which said B cells are isolated.

33. (New) A method according to claim 22, said B cells having been isolated from at least two patients, at least one of whom has recovered from infection by *Clostridium difficile*, and at least one of whom has not recovered from infection by *Clostridium difficile*, said correlation step (ii) correlating the recovery of said at least two patients from infection by *Clostridium difficile*.

34. (New) A method according to claim 22, said B cells having been isolated from at least two patients, said patients being infected by different strains of *Clostridium difficile* producing said at least one antigen, said correlation step (ii) correlating said sequences of at least the VH and/or VL coding regions of said B cells to identify a set of candidate sequences for antibodies, each of which is specific against at least one shared antigen produced by said different strains of *Clostridium difficile* or is specific against different antigens produced by said different strains of *Clostridium difficile*.

35. (New) A method of producing a database which identifies candidate sequences for antibodies specific against at

least one antigen produced by *Clostridium difficile*, comprising the steps of:

- (i) performing a method according to claim 22; and
- (ii) storing the data produced by said method in said database.

36. (New) A method of generating a report which identifies candidate sequences for antibodies specific against at least one antigen produced by *Clostridium difficile*, comprising the steps of:

- (i) performing a method according to claim 22; and
- (ii) producing a report comprising the data produced by said method.